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## RAW SEQUENCE LISTING

DATE: 04/15/2003

PATENT APPLICATION: US/10/018,445A

TIME: 13:55:39

Input Set : A:\10018445.txt

Output Set: N:\CRF4\04152003\J018445A.raw

```

4 <110> APPLICANT: C. Frank Bennett
5      Brett P. Monia
6      Lex M. Cowsert
8 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN BETA 3 EXPRESSION
10 <130> FILE REFERENCE: RTSP-0211
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/018,445A
C--> 12 <141> CURRENT FILING DATE: 2002-08-09
12 <150> PRIOR APPLICATION NUMBER: US 09/344,520
13 <151> PRIOR FILING DATE: 1999-06-25
15 <160> NUMBER OF SEQ ID NOS: 47
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 3170
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
22 <220> FEATURE:
23 <221> NAME/KEY: CDS
24 <222> LOCATION: (21)..(2387)
26 <400> SEQUENCE: 1
27      cgccgcggga ggcggacgag atg cga gcg cgg ccg cgg ccc cgg ccg ctc      50
28                               Met Arg Ala Arg Pro Arg Pro Arg Pro Leu
29                               1             5             10
31      tgg gtg act gtg ctg gcg ctg ggg gcg ctg gcg ggc gtt ggc gta gga      98
32      Trp Val Thr Val Leu Ala Leu Gly Ala Leu Ala Gly Val Gly Val Gly
33                               15             20             25
35      ggg ccc aac atc tgt acc acg cga ggt gtg agc tcc tgc cag cag tgc      146
36      Gly Pro Asn Ile Cys Thr Thr Arg Gly Val Ser Ser Cys Gln Gln Cys
37                               30             35             40
39      ctg gct gtg agc ccc atg tgt gcc tgg tgc tct gat gag gcc ctg cct      194
40      Leu Ala Val Ser Pro Met Cys Ala Trp Cys Ser Asp Glu Ala Leu Pro
41                               45             50             55
43      ctg ggc tca cct cgc tgt gac ctg aag gag aat ctg ctg aag gat aac      242
44      Leu Gly Ser Pro Arg Cys Asp Leu Lys Glu Asn Leu Leu Lys Asp Asn
45      60             65             70
47      tgt gcc cca gaa tcc atc gag ttc cca gtg agt gag gcc cga gta cta      290
48      Cys Ala Pro Glu Ser Ile Glu Phe Pro Val Ser Glu Ala Arg Val Leu
49      75             80             85             90
51      gag gac agg ccc ctc agc gac aag ggc tct gga gac agc tcc cag gtc      338
52      Glu Asp Arg Pro Leu Ser Asp Lys Gly Ser Gly Asp Ser Ser Gln Val
53      95             100             105
55      act caa gtc agt ccc cag agg att gca ctc cgg ctc cgg cca gat gat      386
56      Thr Gln Val Ser Pro Gln Arg Ile Ala Leu Arg Leu Arg Pro Asp Asp
W--> 57      110             115             120
62      tcg aag aat ttc tcc atc caa gtg cgg cag gtg gag gat tac cct gtg      434

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63	Ser Lys Asn Phe Ser Ile Gln Val Arg Gln Val Glu Asp Tyr Pro Val	
W--> 64	125 130 135	
66	gac atc tac tac ttg atg gac ctg tct tac tcc atg aag gat gat ctg	482
67	Asp Ile Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu	
W--> 68	140 145 150	
70	tgg agc atc cag aac ctg ggt acc aag ctg gcc acc cag atg cga aag	530
71	Trp Ser Ile Gln Asn Leu Gly Thr Lys Leu Ala Thr Gln Met Arg Lys	
W--> 72	155 160 165 170	
74	ctc acc agt aac ctg cgg att ggc ttc ggg gca ttt gtg gac aag cct	578
75	Leu Thr Ser Asn Leu Arg Ile Gly Phe Gly Ala Phe Val Asp Lys Pro	
W--> 76	175 180 185	
78	gtg tca cca tac atg tat atc tcc cca cca gag gcc ctc gaa aac ccc	626
79	Val Ser Pro Tyr Met Tyr Ile Ser Pro Pro Glu Ala Leu Glu Asn Pro	
W--> 80	190 195 200	
82	tgc tat gat atg aag acc acc tgc ttg ccc atg ttt ggc tac aaa cac	674
83	Cys Tyr Asp Met Lys Thr Thr Cys Leu Pro Met Phe Gly Tyr Lys His	
W--> 84	205 210 215	
86	gtg ctg acg cta act gac cag gtg acc cgc ttc aat gag gaa gtg aag	722
87	Val Leu Thr Leu Thr Asp Gln Val Thr Arg Phe Asn Glu Glu Val Lys	
W--> 88	220 225 230	
90	aag cag agt gtg tca cgg aac cga gat gcc cca gag ggt ggc ttt gat	770
91	Lys Gln Ser Val Ser Arg Asn Arg Asp Ala Pro Glu Gly Gly Phe Asp	
W--> 92	235 240 245 250	
94	gcc atc atg cag gct aca gtc tgt gat gaa aag att ggc tgg agg aat	818
95	Ala Ile Met Gln Ala Thr Val Cys Asp Glu Lys Ile Gly Trp Arg Asn	
W--> 96	255 260 265	
98	gat gca tcc cac ttg ctg gtg ttt acc act gat gcc aag act cat ata	866
99	Asp Ala Ser His Leu Leu Val Phe Thr Thr Asp Ala Lys Thr His Ile	
W--> 100	270 275 280	
102	gca ttg gac gga agg ctg gca ggc att gtc cag cct aat gac ggg cag	914
103	Ala Leu Asp Gly Arg Leu Ala Gly Ile Val Gln Pro Asn Asp Gly Gln	
W--> 104	285 290 295	
106	tgt cat gtt ggt agt gac aat cat tac tct gcc tcc act acc atg gat	962
107	Cys His Val Gly Ser Asp Asn His Tyr Ser Ala Ser Thr Thr Met Asp	
W--> 108	300 305 310	
110	tat ccc tct ttg ggg ctg atg act gag aag cta tcc cag aaa aac atc	1010
111	Tyr Pro Ser Leu Gly Leu Met Thr Glu Lys Leu Ser Gln Lys Asn Ile	
W--> 112	315 320 325 330	
114	aat ttg atc ttt gca gtg act gaa aat gta gtc aat ctc tat cag aac	1058
115	Asn Leu Ile Phe Ala Val Thr Glu Asn Val Val Asn Leu Tyr Gln Asn	
W--> 116	335 340 345	
118	tat agt gag ctc atc cca ggg acc aca gtt ggg gtt ctg tcc atg gat	1106
119	Tyr Ser Glu Leu Ile Pro Gly Thr Thr Val Gly Val Leu Ser Met Asp	
W--> 120	350 355 360	
122	tcc agc aat gtc ctc cag ctc att gtt gat gct tat ggg aaa atc cgt	1154
123	Ser Ser Asn Val Leu Gln Leu Ile Val Asp Ala Tyr Gly Lys Ile Arg	
W--> 124	365 370 375	
126	tct aaa gtc gag ctg gaa gtg cgt gac ctc cct gaa gag ttg tct cta	1202
127	Ser Lys Val Glu Leu Glu Val Arg Asp Leu Pro Glu Glu Leu Ser Leu	

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W--> 128	380	385	390	
130	tcc ttc aat gcc acc tgc ctc aac aat gag gtc atc cct ggc ctc aag			1250
131	Ser Phe Asn Ala Thr Cys Leu Asn Asn Glu Val Ile Pro Gly Leu Lys			
W--> 132	395	400	405	410
134	tct tgt atg gga ctc aag att gga gac acg gtg agc ttc agc att gag			1298
135	Ser Cys Met Gly Leu Lys Ile Gly Asp Thr Val Ser Phe Ser Ile Glu			
W--> 136	415	420	425	
138	gcc aag gtg cga ggc tgt ccc cag gag aag gag aag tcc ttt acc ata			1346
139	Ala Lys Val Arg Gly Cys Pro Gln Glu Lys Glu Lys Ser Phe Thr Ile			
W--> 140	430	435	440	
142	aag ccc gtg ggc ttc aag gac agc ctg atc gtc cag gtc acc ttt gat			1394
143	Lys Pro Val Gly Phe Lys Asp Ser Leu Ile Val Gln Val Thr Phe Asp			
W--> 144	445	450	455	
146	tgt gac tgt gcc tgc cag gcc caa gct gaa cct aat agc cat cgc tgc			1442
147	Cys Asp Cys Ala Cys Gln Ala Gln Ala Glu Pro Asn Ser His Arg Cys			
W--> 148	460	465	470	
150	aac aat ggc aat ggg acc ttt gag tgt ggg gta tgc cgt tgt ggg cct			1490
151	Asn Asn Gly Asn Gly Thr Phe Glu Cys Gly Val Cys Arg Cys Gly Pro			
W--> 152	475	480	485	490
154	ggc tgg ctg gga tcc cag tgt gag tgc tca gag gag gac tat cgc cct			1538
155	Gly Trp Leu Gly Ser Gln Cys Glu Cys Ser Glu Glu Asp Tyr Arg Pro			
W--> 156	495	500	505	
158	tcc cag cag gac gag tgc agc ccc cga gag ggt cag ccc gtc tgc agc			1586
159	Ser Gln Gln Asp Glu Cys Ser Pro Arg Glu Gly Gln Pro Val Cys Ser			
W--> 160	510	515	520	
162	cag cgg ggc gag tgc ctc tgt ggt caa tgt gtc tgc cac agc agt gac			1634
163	Gln Arg Gly Glu Cys Leu Cys Gly Gln Cys Val Cys His Ser Ser Asp			
W--> 164	525	530	535	
166	ttt ggc aag atc acg ggc aag tac tgc gag tgt gac gac ttc tcc tgt			1682
167	Phe Gly Lys Ile Thr Gly Lys Tyr Cys Glu Cys Asp Asp Phe Ser Cys			
W--> 168	540	545	550	
170	gtc cgc tac aag ggg gag atg tgc tca ggc cat ggc cag tgc agc tgt			1730
171	Val Arg Tyr Lys Gly Glu Met Cys Ser Gly His Gly Gln Cys Ser Cys			
W--> 172	555	560	565	570
174	ggg gac tgc ctg tgt gac tcc gac tgg acc ggc tac tac tgc aac tgt			1778
175	Gly Asp Cys Leu Cys Asp Ser Asp Trp Thr Gly Tyr Tyr Cys Asn Cys			
W--> 176	575	580	585	
178	acc acg cgt act gac acc tgc atg tcc agc aat ggg ctg ctg tgc agc			1826
179	Thr Thr Arg Thr Asp Thr Cys Met Ser Ser Asn Gly Leu Leu Cys Ser			
W--> 180	590	595	600	
182	ggc cgc ggc aag tgt gaa tgt ggc agc tgt gtc tgt atc cag ccg ggc			1874
183	Gly Arg Gly Lys Cys Glu Cys Gly Ser Cys Val Cys Ile Gln Pro Gly			
W--> 184	605	610	615	
186	tcc tat ggg gac acc tgt gag aag tgc ccc acc tgc cca gat gcc tgc			1922
187	Ser Tyr Gly Asp Thr Cys Glu Lys Cys Pro Thr Cys Pro Asp Ala Cys			
W--> 188	620	625	630	
190	acc ttt aag aaa gaa tgt gtg gag tgt aag aag ttt gac cgg gag ccc			1970
191	Thr Phe Lys Lys Glu Cys Val Glu Cys Lys Lys Phe Asp Arg Glu Pro			
W--> 192	635	640	645	650

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```

194   tac atg acc gaa aat acc tgc aac cgt tac tgc cgt gac gag att gag      2018
195   Tyr Met Thr Glu Asn Thr Cys Asn Arg Tyr Cys Arg Asp Glu Ile Glu
W--> 196               655               660               665
198   tca gtg aaa gag ctt aag gac act ggc aag gat gca gtg aat tgt acc      2066
199   Ser Val Lys Glu Leu Lys Asp Thr Gly Lys Asp Ala Val Asn Cys Thr
W--> 200               670               675               680
202   tat aag aat gag gat gac tgt gtc gtc aga ttc cag tac tat gaa gat      2114
203   Tyr Lys Asn Glu Asp Asp Cys Val Val Arg Phe Gln Tyr Tyr Glu Asp
W--> 204               685               690               695
206   tct agt gga aag tcc atc ctg tat gtg gta gaa gag cca gag tgt ccc      2162
207   Ser Ser Gly Lys Ser Ile Leu Tyr Val Val Glu Glu Pro Glu Cys Pro
W--> 208               700               705               710
210   aag ggc cct gac atc ctg gtg gtc ctg ctc tca gtg atg ggg gcc att      2210
211   Lys Gly Pro Asp Ile Leu Val Val Leu Leu Ser Val Met Gly Ala Ile
W--> 212               715               720               725               730
214   ctg ctc att ggc ctt gcc gcc ctg ctc atc tgg aaa ctc ctc atc acc      2258
215   Leu Leu Ile Gly Leu Ala Ala Leu Leu Ile Trp Lys Leu Leu Ile Thr
W--> 216               735               740               745
218   atc cac gac cga aaa gaa ttc gct aaa ttt gag gaa gaa cgc gcc aga      2306
219   Ile His Asp Arg Lys Glu Phe Ala Lys Phe Glu Glu Glu Arg Ala Arg
W--> 220               750               755               760
222   gca aaa tgg gac aca gcc aac aac cca ctg tat aaa gag gcc acg tct      2354
223   Ala Lys Trp Asp Thr Ala Asn Asn Pro Leu Tyr Lys Glu Ala Thr Ser
W--> 224               765               770               775
226   acc ttc acc aat atc acg tac cgg ggc act taa tgataagcag tcatcctcag      2407
227   Thr Phe Thr Asn Ile Thr Tyr Arg Gly Thr
W--> 228               780               785
230   atcattatca gcctgtgccg ggattgcagg agtccctgcc atcatgttta cagaggacag      2467
232   tatttgtggg gagggatttc ggggctcaga gtggggtagg ttgggagaat gtcagtatgt      2527
234   ggaagtgtgg gtctgtgtgt gtgtatgtgg gggctgtgtg gtttatgtgt gtgtgttgtg      2587
236   tgtgggagtg tgtaatttaa aattgtgatg tgtcctgata agctgagctc cttagccttt      2647
238   gtcccagaat gcctcctgca gggattcttc ctgcttagct tgaggggtgac tatggagctg      2707
240   agcaggtgtt cttcattacc tcagttagaa gccagcttcc ctcattcaggc cattgtccct      2767
242   gaagagaagg gcagggctga ggcctctcat tccagaggaa gggacaccaa gccttggctc      2827
244   taccctgagt tcataaattt atggttctca ggcctgactc tcagcagcta tggtaggaac      2887
246   tgctggcttg gcagcccggg tcattctgtac ctctgcctcc tttccctccc ctcaggccga      2947
248   aggaggagtc agggagagct gaactattag agctgcctgt gccttttgcc atcccctcaa      3007
250   cccagctatg gttctctcgc aagggaagtc cttgcaagct aattctttga cctgttgga      3067
252   gtgaggatgt ctgggccact caggggtcat tcatggcctg ggggatgtac cagcatctcc      3127
254   cagttcataa tcacaaccct tcagatttgc cttattggca gcg                        3170
257 <210> SEQ ID.NO: 2
258 <211> LENGTH: 23
259 <212> TYPE: DNA
260 <213> ORGANISM: Artificial Sequence
262 <220> FEATURE:
263 <223> OTHER INFORMATION: PCR Primer
265 <400> SEQUENCE: 2
266   tttaccactg atgccaagac tca
269 <210> SEQ ID NO: 3

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```

270 <211> LENGTH: 21
271 <212> TYPE: DNA
272 <213> ORGANISM: Artificial Sequence
274 <220> FEATURE:
275 <223> OTHER INFORMATION: PCR Primer
277 <400> SEQUENCE: 3
278      ccgtcattag gctggacaat g                                21
281 <210> SEQ ID NO: 4
282 <211> LENGTH: 25
283 <212> TYPE: DNA
284 <213> ORGANISM: Artificial Sequence
286 <220> FEATURE:
287 <223> OTHER INFORMATION: PCR Probe
289 <400> SEQUENCE: 4
290      atagcattgg acggaaggct ggcag                                25
293 <210> SEQ ID NO: 5
294 <211> LENGTH: 19
295 <212> TYPE: DNA
296 <213> ORGANISM: Artificial Sequence
298 <220> FEATURE:
299 <223> OTHER INFORMATION: PCR Primer
301 <400> SEQUENCE: 5
302      gaaggtgaag gtcggagtc                                    19
305 <210> SEQ ID NO: 6
306 <211> LENGTH: 20
307 <212> TYPE: DNA
308 <213> ORGANISM: Artificial Sequence
310 <220> FEATURE:
311 <223> OTHER INFORMATION: PCR Primer
313 <400> SEQUENCE: 6
314      gaagatggtg atgggatttc                                    20
317 <210> SEQ ID NO: 7
318 <211> LENGTH: 20
319 <212> TYPE: DNA
320 <213> ORGANISM: Artificial Sequence
322 <220> FEATURE:
323 <223> OTHER INFORMATION: PCR Probe
325 <400> SEQUENCE: 7
326      caagcttccc gttctcagcc                                    20
329 <210> SEQ ID NO: 8
330 <211> LENGTH: 18
331 <212> TYPE: DNA
332 <213> ORGANISM: Artificial Sequence
334 <220> FEATURE:
335 <223> OTHER INFORMATION: Antisense Oligonucleotide
337 <400> SEQUENCE: 8
338      gcatctcgtc cgctcccc                                    18
341 <210> SEQ ID NO: 9
342 <211> LENGTH: 18

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/018,445A

DATE: 04/15/2003

TIME: 13:55:40

Input Set : A:\10018445.txt

Output Set: N:\CRF4\04152003\J018445A.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:57 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:64 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:68 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:72 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:76 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:80 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:84 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:88 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:92 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:96 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:100 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:104 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:112 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:116 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:120 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:124 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:128 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:132 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:136 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:140 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:144 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:148 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:152 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:156 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:160 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:164 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:168 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:172 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:176 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:180 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:184 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:188 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
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L:196 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:200 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:204 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:208 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:212 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:216 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:220 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:224 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:228 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1